RAW SEQUENCE LISTING
ERROR REPORT
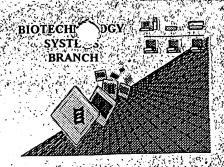
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/484,629_

Source: _1711_

Date Processed by STIC: _5-14-01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY; or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT WITH A NOTICE TO COMPLY.
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION   SERIAL NUMBER: _09/484, 625_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
                                 This may occur if your file was retrieved in a word processor after creating it.
                                 Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
                                 This may occur if your file was retrieved in a word processor after creating it.
                                 Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
         Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
                                 Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
                                 As per the rules, each n or Xaa can only represent a single residue.
                                 Please present the maximum number of each residue having variable length and
                                 indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
                                 sequence(s) _____. Normally, PatentIn would automatically generate this section from the
                                 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
                                 to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>**
                                 sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
         (OLD RULES)   **(2) INFORMATION FOR SEQ ID NO:X:**
                                 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
                                 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
                                 This sequence is intentionally skipped

                                 Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
         (NEW RULES)   **<210> sequence id number**
                                 <400> sequence id number
                                 000

10 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
         (NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
                                 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 __✓__ Use of "Artificial"   Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
         (NEW RULES)   Valid response is Artificial Sequence.

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
         (NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
                                 Please explain source of genetic material in <220> to <223> section.
                                 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
                                 file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
                                 Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

S. Acquah (handwritten)

RAW SEQUENCE LISTING *9* (handwritten) DATE: 05/14/2001
PATENT APPLICATION: US/09/484,625 TIME: 11:53:16

Input Set : A:\list5-2-01.ST25.txt
Output Set: N:\CRF3\05142001\I484625.raw

Does Not Comply (handwritten)
Corrected Diskette Needed (handwritten)
See p. 5 (handwritten)

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  3 <110> APPLICANT: Medical Research Council
  5 <120> TITLE OF INVENTION: Obesity gene
  7 <130> FILE REFERENCE: 18396/1140
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/484,625
 10 <141> CURRENT FILING DATE: 2000-01-18
 12 <150> PRIOR APPLICATION NUMBER: PCT/GB99/02658
 13 <151> PRIOR FILING DATE: 1998-12-08
 15 <160> NUMBER OF SEQ ID NOS: 37
 17 <170> SOFTWARE: PatentIn version 3.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 924
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Rattus sp.
 24 <400> SEQUENCE: 1
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 27 gctccttctg cccgtgcgcg gccgcaagac ccgcctgcca agtccaaggt              120
 29 cgggcgcgtg aaaatgcctc ctgcagtgga ccctgcggaa ttgttcgtgt tgaccgagcg   180
 31 ctaccgacag taccgggaga cggtgcgcgc tctcaggcga gagttcacat tggaggtgcg   240
 33 agggaaattg cacgaggccc gagccgggct tctggctgag cgcaaggcgc aagaggccat   300
 35 cagagagcac caggagctga tggcctggaa ccgggaggag aaccggagac tgcaggaact   360
 37 acggatagct aggttgcagc tcgaagcaca ggcccaggag ctgcggcagg ctgaggtcca   420
 39 ggcccagagg gcccaggagg agcaggcttg ggtgcaactg aaagaacaag aagttctcaa   480
 41 actgcaggag gaggccaaaa acttcatcac tcgggagaac ctggaggcac ggatagaaga   540
 43 ggccttggac tctccgaaga gttataactg ggcggtcacc aaagaagggc aggtggtcag   600
 45 gaactgagaa cagaggcctc tcaggcccaa ataaggacag tgcttgccta gggactggat   660
 47 attggggtag aaattggtgc atcccaggag ggtggcacag ccttgtccag agcagccccc   720
 49 attcattcta gatttggcac caggtatagt acctgttctg acaccacata caaactccgg   780
 51 acagcattaa actctgggaa gttcctatca cacagaagat cagactggac tgtcccctct   840
 53 agaagccaag agctgtctcc tgagtttctt ggaatagtgt gagcccaatg tttcctgctt   900
 55 ttataaataa actattggaa agca                                         924
 58 <210> SEQ ID NO: 2
 59 <211> LENGTH: 200
 60 <212> TYPE: PRT
 61 <213> ORGANISM: Rattus sp.
 63 <400> SEQUENCE: 2
 65 Met Leu Arg Ala Leu Asn Arg Leu Ala Ala Arg Pro Gly Gly Gln Pro
 66  1               5                  10               15
 68 Pro Thr Leu Leu Leu Leu Pro Val Arg Gly Arg Leu Thr Arg His Asp
 69              20                  25               30
 71 Pro Pro Ala Leu Ser Leu Val Gly Arg Val Leu Met Pro Pro Ala Val
 72          35                  40               45
 74 Asp Pro Ala Glu Leu Phe Val Leu Thr Glu Arg Tyr Arg Gln Tyr Arg
 75          50                  55               60
 77 Glu Thr Val Arg Ala Leu Arg Arg Glu Phe Thr Leu Glu Val Arg Gly
 78 65                  70                  75               80
 80 Lys Leu His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Gln
 81                  85                  90               95
```

```
83  Glu Ala Ile Arg Glu His Gln Glu Leu Met Ala Trp Asn Arg Glu Glu
84          100                 105                 110
86  Asn Arg Arg Leu Gln Glu Leu Arg Ile Ala Arg Leu Gln Leu Glu Ala
87          115                 120                 125
89  Gln Ala Gln Glu Leu Arg Gln Ala Glu Val Gln Ala Gln Arg Ala Gln
90      130                 135                 140
92  Glu Glu Gln Ala Trp Val Gln Leu Lys Glu Gln Glu Val Leu Lys Leu
93  145                 150                 155                 160
95  Gln Glu Glu Ala Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg
96                  165                 170                 175
98  Ile Glu Glu Ala Leu Asp Ser Pro Lys Ser Tyr Asn Trp Ala Val Thr
99                  180                 185                 190
101 Lys Glu Gly Gln Val Val Arg Asn
102         195                 200
104 <210> SEQ ID NO: 3
105 <211> LENGTH: 998
106 <212> TYPE: DNA
107 <213> ORGANISM: Rattus sp.
109 <400> SEQUENCE: 3
110 atgctacgcg cgctgagccg cctgggcgcg gggaccccgt gcaggccccg ggcccctctg    60
112 gtgctgccag cgcgcggccg caagacccgc cacgacccgc tggccaaatc caagatcgag   120
114 cgagtgaaca tgccgcccgc ggtgggaccct gcggagttct tcgtgctgat ggagcgttac   180
116 cagcactacc gccagac\cgt gcgcgccctc aggatggagt tcgtgtccga ggtgcagagg   240
118 aaggtgcacg aggcccgagc cggggttctg gcggagcgca aggccctgaa ggacgccgcc   300
120 gagcaccgcg agctgatggc ctggaaccag gcggagaacc ggcggctgca cgagctgcgg   360
122 atagcgaggc tgcggcagga ggagcgggag caggagcagc ggcaggcgtt ggagcaggcc   420
124 cgcaaggccg aagaggtgca ggcctgggcg cagcgcaagg agcgggaagt gctgcagctg   480
126 caggaagagg tgaaaaactt catcacccga gagaacctgg aggcacgggt ggaagcagca   540
128 ttggactccc ggaagaacta caactgggcc atcaccagag aggggctggt ggtcaggcca   600
130 caacgcaggg actcctaggg gcccagtaag gacagtgccc gccagggacc atgtatgtat   660
132 catggcggaa gagttggccc tgacctggaa taaagcagtt ggtgttgctt atgaggaagg   720
134 ttcagcctta tccagcacag ccttcacgtt ttgccctctg ctgtcaccac ttggtcagaa   780
136 acttccaaac gcagtgccct gttctgccgg tgtgtaaagc ctcagcgcac caggagaccc   840
138 tagagtggtt tccatctcac agagaatcag acaggccaca gcccctcag gcagccaggt   900
140 catctgagta tcattaagag tagtgatggg aagattacag tctgagggcc aaacgtgcct   960
142 gcttcctgtt tttgtaaata aagttttgtt ggaacaca                           998
145 <210> SEQ ID NO: 4
146 <211> LENGTH: 205
147 <212> TYPE: PRT
148 <213> ORGANISM: Rattus sp.
150 <400> SEQUENCE: 4
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153 1               5               10                  15
155 Arg Ala Pro Leu Val Leu Pro Ala Arg Gly Arg Lys Thr Arg His Asp
156         20                  25                  30
158 Pro Leu Ala Lys Ser Lys Ile Glu Arg Val Asn Met Pro Pro Ala Val
159         35                  40                  45
161 Asp Pro Ala Glu Phe Phe Val Leu Met Glu Arg Tyr Gln His Tyr Arg
162     50                  55                  60
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Input Set : A:\list5-2-01.ST25.txt
Output Set: N:\CRF3\05142001\I484625.raw

```
164 Gln Thr Val Arg Ala Leu Arg Met Glu Phe Val Ser Glu Val Gln Arg
165 65               70              75              80
167 Lys Val His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Leu
168               85              90              95
170 Lys Asp Ala Ala Glu His Arg Glu Leu Met Ala Trp Asn Gln Ala Glu
171               100             105             110
173 Asn Arg Arg Leu His Glu Leu Arg Ile Ala Arg Leu Arg Gln Glu Glu
174         115             120             125
176 Arg Glu Gln Glu Gln Arg Gln Ala Leu Glu Gln Ala Arg Lys Ala Glu
177     130             135             140
179 Glu Val Gln Ala Trp Ala Gln Arg Lys Glu Arg Glu Val Leu Gln Leu
180 145             150             155             160
182 Gln Glu Glu Val Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg
183               165             170             175
185 Val Glu Ala Ala Leu Asp Ser Arg Lys Asn Tyr Asn Trp Ala Ile Thr
186               180             185             190
188 Arg Glu Gly Leu Val Val Arg Pro Gln Arg Arg Asp Ser
189         195             200             205
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191 <210> SEQ ID NO: 5
192 <211> LENGTH: 943
193 <212> TYPE: DNA
194 <213> ORGANISM: Mus musculus

196 <400> SEQUENCE: 5

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199 gctgctcctg cccgtgcgcg gccgcaagac ccgccatgac ccgcctgcca aatccaaggt   120
201 cggacgggtg cagacgcctc ccgccgtgga ccctgcggaa ttcttcgtgt tgaccgagcg   180
203 ctacggacag taccgggaga ccgtgcgcgc tctcaggcta gagttcacgt tggatgtgcg   240
205 aaggaaattg cacgaggccc gagccggggt tctggccgag cgcaaggcgc agcaggccat   300
207 cacggagcac cgggagctga tggcctggaa ccgggacgag aaccggcgaa tgcaggagct   360
209 acggatagcg aggttgcagc tggaagcaca ggcccaggag gtgcagaagg ctgaggccca   420
211 gcgccagagg gctcaggagg agcaggcttg ggtgcaactg aaagagcaag aagtgctcaa   480
213 gctgcaggag gaggcaaaaa acttcatcac tcgggagaac ctggaggcac ggatagaaga   540
215 agcgttggac tctccgaaga gttacaactg ggccgtcacc aaagaagggc aggtggtcag   600
217 gaactgagca cagagacttc tggggggccca ataagcaca gtgcttgcct agggtctgtg   660
219 tactgggata ggaattggta catcccagga ggatggctca gccgtttcca gagcaacctc   720
221 agtcactcca ggctcggcac tcaccacctg actgggaact cccagatgtc cctgttctgg   780
223 caccacagtc aaactgaggg cagcattaaa ctctgggaag ttcctatcgc acagaggatc   840
225 ggactggact gtgtccctct agaagccaag cttgtcttgt aagtctcttg gagtcctgtg   900
227 agccaaatgt ttcctgcttt tataaataaa gtattggagc cca                     943
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230 <210> SEQ ID NO: 6
231 <211> LENGTH: 200
232 <212> TYPE: PRT
233 <213> ORGANISM: Mus musculus

235 <400> SEQUENCE: 6

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237 Met Leu Arg Ala Leu Asn Arg Leu Ala Gln Arg Pro Gly Asp Arg Pro
238 1               5               10              15
240 Pro Thr Pro Leu Leu Leu Pro Val Arg Gly Arg Lys Thr Arg His Asp
241               20              25              30
243 Pro Pro Ala Lys Ser Lys Val Gly Arg Val Gln Thr Pro Pro Ala Val
```

```
244          35                    40                   45
246 Asp Pro Ala Glu Phe Phe Val Leu Thr Glu Arg Tyr Gly Gln Tyr Arg
247      50                    55                   60
249 Glu Thr Val Arg Ala Leu Arg Leu Glu Phe Thr Leu Asp Val Arg Arg
250 65                    70                   75                   80
252 Lys Leu His Glu Ala Arg Ala Gly Val Leu Ala Glu Arg Lys Ala Gln
253                  85                   90                   95
255 Gln Ala Ile Thr Glu His Arg Glu Leu Met Ala Trp Asn Arg Asp Glu
256              100                  105                  110
258 Asn Arg Arg Met Gln Glu Leu Arg Ile Ala Arg Leu Gln Leu Glu Ala
259          115                  120                  125
261 Gln Ala Gln Glu Val Gln Lys Ala Glu Ala Gln Arg Gln Arg Ala Gln
262      130                  135                  140
264 Glu Glu Gln Ala Trp Val Gln Leu Lys Glu Gln Glu Val Leu Lys Leu
265 145                  150                  155                  160
267 Gln Glu Glu Ala Lys Asn Phe Ile Thr Arg Glu Asn Leu Glu Ala Arg
268              165                  170                  175
270 Ile Glu Glu Ala Leu Asp Ser Pro Lys Ser Tyr Asn Trp Ala Val Thr
271          180                  185                  190
273 Lys Glu Gly Gln Val Val Arg Asn
274          195                  200
276 <210> SEQ ID NO: 7
277 <211> LENGTH: 2852
278 <212> TYPE: DNA
279 <213> ORGANISM: Homo sapiens
281 <400> SEQUENCE: 7
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284 ctgtgcaagg aaggatggag tgcacgttcc ctgatgttca gagcaaccct gtgtcactcc   120
286 aggtaggtga gatgagagga agagggtggc cttggcctgg gcctcctacg ggcctggaag   180
288 ttgggagaag gatgtaagca gactctgttc tcttctgaga aatatcaggt attgcagtca   240
290 gcccaggctc ctcagaccct cctaagtgca gattctctgc agaatctggt gttgacaaca   300
292 ctaatgagta ggatgagact tcagttccct agccctcacc gtcagcttct gattaccaac   360
294 aactctccca gaggagagcc atctaccttt gggacagatg ctctctgccc tgcactgcct   420
296 cctgtttctc ttcattgtag aggaagatag tactttaaaa gcttcataaa tggtctcaag   480
298 gtgggaagac cccggctcag gtgaaagagg acaagcgtca cctcacacag gccacccagt   540
300 agaaaacaag tgatcactga tactgagaac tctggcaatt gcagagctgc ccaagaccac   600
302 aacagggcag tgcaatgcaa ggaaaaggtt tgttgctcga ttgcaaacct aaagtttaaa   660
304 gtgcatcagg agaacgctta ctcaaagagg aagtgtaagc ctaacttaag tagctagaag   720
306 ctcagaattt cttgcatcag ccctggaagg gtacacaggc caccggtggg ccagagaacc   780
308 acacgctttg gggcggtgtc caagcttgtg aacaagtagg caagagcgcc tggtgttgta   840
310 gctgtcattg gcgggcaata cagcccagcg aactgtggtc tccaaggtgc ccctcgaccc   900
312 tcccactcta cccgagactc cagggacgcg atgggccaga cagcaagagc tccgcctacg   960
314 ggggcgggga caggagattc ccgtgatgct cctcgaccac ttccggacag ggcgcaggcg  1020
316 ctagctgtca tgttgcgggc tttgaaccgc ctggccgcgc ggcccggggg ccagcccccа  1080
318 accctgctcc ttctgcccgt gcgcggccca cggccccgct cattctcggc tcctttttcc  1140
320 tcgcaggata gctaggttgc agctcgaagc acaggcccag gagctgcggc aggctgaggt  1200
322 ccaggcccag agggcccagg aggagcaggc ttgggtgcaa ctgaaagaac aagaagttct  1260
324 caaactgcag gtgggccgag gtcgtgagga atgtgggtat ggagattcc ggtgagggag  1320
326 gctctgggga gagcagcaca gggtgtcaag tgaccagtct tcaggaggct tctctctctg  1380
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RAW SEQUENCE LISTING   DATE: 05/14/2001
PATENT APPLICATION: US/09/484,625   TIME: 11:53:17

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Output Set: N:\CRF3\05142001\I484625.raw

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330 ccgtgtgaaa cttgaaggtc agggaaacca taaatgagaa tggagctgtt tttattgtgt   1500
332 aagggagagt gacaaggttg agagagtcca ccaccccgca cctcccccg ccccaatca    1560
334 ggttgtcacg attcgattcg ttcttgggtt gtggctgaga gatctgatgg gtaattgtcc   1620
336 gaggaagagg gatataatgg ttgaggtcac ctagtacagt tgtgctggcc tattggtggg   1680
338 acactcaaag gggccctggg ctcttttgac acccttctta aggtgggcta gagacagtaa   1740
340 gttatgcagg cagccagctc tgagagatcc cacgtagcta acctttctct tcccgtagga   1800
342 ggaggccaaa aacttcatca ctcgggagaa cctggaggca cggatagaag aggccttgga   1860
344 ctctccgaag agttataact gggcggtcac caaagaaggg caggtggtca ggaactgaga   1920
346 acagaggcct ctcaggccca aataaggaca gtgcttgcct agggactgga tattggggta   1980
348 gaaattggtg catcccagga gggtggcaca gccttgtcca gagcagcccc cattcattct   2040
350 agatttggca ccaggtatag tacctgttct gacaccacat acaaactccg gacagcatta   2100
352 aactctggga agttcctatc acacagaaga tcagactgga ctgtcccctc tagaagccaa   2160
354 gagctgtctc ctgagtttct tggaatagtg tgagcccaat gtttcctgct tttataaata   2220
356 aactattgga aagcaaagcc ttttgttatg tggcttgctt tttcttgttg tagaataagt   2280
358 ttatttgtcc cagttatttg ggtcttaagg ttattagcca aaagccagtt cacctaactg   2340
360 agccaggagt tagttatctg ctttgctcaa tcctgggctt tgctgggtag ggtcaggtgt   2400
362 gtccaaggtc cagaaagcaa aaagggtgcc ccgtttctcc tgggaaggct tccccgtcag   2460
364 tgatttctgt aaccggaccc tgccctgaca cagcgtcatt ggactaccca gcagacagta   2520
366 gactccactc taaacccgct tcttgcggtc agttgctgtc cttcagtgtg tgtaagcagt   2580
368 ggccagacag cacccttggg tgtcatttca agactctctc accttggtct gctttacgtt   2640
370 tggtttgatt tggtttgttc tggtttttga gacgaggcct ttcactggaa cctggcactc   2700
372 agtatttaga ctgcccagcc agctagcctc agagaatgca tctgcgtatg cttgcctggc   2760
374 gctggaattc ggtgcacatg gctttgatgt gtaccgggga tcagacacag atgtttcatg   2820
376 agtgcagtgc atgcctgtta gtggtagagc tc                                 2852
379 <210> SEQ ID NO: 8
380 <211> LENGTH: 41
381 <212> TYPE: PRT
382 <213> ORGANISM: Homo sapiens
384 <400> SEQUENCE: 8
386 Met Leu Arg Ala Leu Asn Arg Leu Ala Ala Arg Pro Gly Gly Gln Pro
387 1               5                   10                  15
389 Pro Thr Leu Leu Leu Leu Pro Val Arg Gly Pro Arg Pro Arg Ser Phe
390             20                  25                  30
392 Ser Ala Pro Phe Ser Ser Gln Asp Ser
393         35                  40
395 <210> SEQ ID NO: 9
396 <211> LENGTH: 20
397 <212> TYPE: DNA
398 <213> ORGANISM: (Artificial)
400 <220> FEATURE:
401 <223> OTHER INFORMATION: SYNTHETIC PRIMER
403 <220> FEATURE:
404 <221> NAME/KEY: misc_feature
405 <222> LOCATION: (1)..(20)
406 <223> OTHER INFORMATION: SYNTHETIC PRIMER
409 <400> SEQUENCE: 9
410 ttcacaccac tctgtcgaac                                                20
413 <210> SEQ ID NO: 10
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C--> *(handwritten annotation pointing to line 398)*

Handwritten note: Incomplete <213> response as per Section 1.823b of the new sequence rules. See #11 on the Error Summary Sheet.

Handwritten: Please Note:

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY DATE: 05/14/2001
PATENT APPLICATION: US/09/484,625 TIME: 11:53:18

Input Set : A:\list5-2-01.ST25.txt
Output Set: N:\CRF3\05142001\I484625.raw

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:398 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:416 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
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